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Conference Abstract

Phylogenetics Study of *Salvia* L. spp. Collections from the Botanical Garden of Medicinal Plants of Wroclaw Medical University

Bartosz Pencakowski[‡], Monika Bielecka[‡], Marta Stafiniak[‡], Klemens Jakubowski[§], Adam Matkowski[|]

‡ Department of Pharmaceutical Biotechnology, Wrocław Medical University, Wroclaw, Poland
§ Botanical Garden of Medicinal Plants, Wroclaw Medical University, Wroclaw, Poland
| Department of Biology and Pharmaceutical Botany, Wroclaw Medical University, Wroclaw, Poland

Corresponding author: Bartosz Pencakowski (bartosz.pencakowski@umed.wroc.pl)

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Abstract

Systematics of genus *Salvia* L. is still a field of discussion in taxonomic society. To this day, the position of certain genera from *Lamiaceae* Martinov. family are considered as autonomic genera or incorporated in the genus *Salvia* L. as a subgenera (i.e., *Perovskia* Kar., *Rosmarinus* L.). Moreover, some species are distinguished only by low-level differences in morphological traits and their geographic occurrence (Drew et al. 2017).

In this research, we focused on a molecular analysis of morphologically similar *Salvia* L. species with special attention paid to *Salvia glutinosa* L. and *Salvia nubicola* Wall. ex Sweet. All samples were collected from the Botanical Garden of Medicinal Plants of Wroclaw Medical University (http://www.obrl.umed.wroc.pl/index.html) and the Herbarium of Natural History Museum, Wroclaw University (http://www.muzeum-przyrodnicze.uni.wroc.pl/index.php).

Several DNA barcodes, including *mat*K, *rbc*La, ITS2 genes, and *psb*A-*trn*H intergenic spacer, were used in maximal likelihood and Bayesian inference analyses. All sequences were amplified with Q5 High Fidelity DNA Polymerase (https://www.neb.com/) and

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universal primers. Amplicons were then sequenced by Sanger sequencing and analysed using the BLAST algorithm (Altschul et al. 1990). Subsequently, sequences were aligned using MAFFT v 7.409 (Katoh et al. 2005) software; poorly aligned sites were objectively eliminated with Gblocks v.0.91b (Talavera and Castresana 2007). ITS2 regions were extracted with ITSx (Bengtsson-Palme et al. 2013) software implemented on PlutoF web workbench (Abarenkov et al. 2010) to obtain ITS2 sequences without 5.8S and 26S fragments on both ends. Substitution models were identified utilizing jModelTest 2 software (Posada 2008) and basing on Bayesian information criterion (BIC) appropriate models were applied for further calculations. For maximum likelihood analyses and Bayesian inference, we implemented RAxML ver. 8.2.10 (Stamatakis et al. 2008) and MrBayes ver. 3.2.2 (Ronquist et al. 2012) respectively.

For the reconstruction of evolutionary relationship between study species, different DNA barcode combinations were applied (e.g., *mat*K+ITS2+*psb*A-*trn*H and *rbc*La+*mat*K+ *psb*A-*trn*H). Consensus trees were compared and analysed using TreeGraph ver. 2.14 (Stöver and Müller 2010).

Keywords

DNA barcoding, *Salvia*, phylogenetics

Presenting author

Bartosz Pencakowski

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